**Amendments to the Specification:**

Please insert the enclosed paper copy of the sequence listing into the application after the section entitled "Abstract of the Disclosure."

Please replace paragraph [0016] bridging pages 7 and 8 of the application with the following amended paragraph:

--Fig. 2. GLD-2 belongs to the polβ nucleotidyltransferase superfamily. Fig. 2a: The polβ superfamily (adapted from Kadyk and Kimble, J., supra, 1998). Small color-coded circles represent sub-families; grey circle shows Group 2 families. Most important here are the eukaryotic TRF, TRF4/5-related proteins; PAP, eukaryotic poly(A) polymerase; and 2'-5'A, 2'-5' oligoA synthetase. Fig. 2b-d: Color coding of domains based on crystal structures of bovine and yeast PAPs (Martin, G., et al., supra, 2000; Bard, J., et al., supra, 2000). Gold, catalytic domain; blue, central domain; violet, RRM domain. Fig. 2b: GLD-2 and PAP domains compared. *Drosophila* (Dm), human (Hs) and yeast (Sc). GLD-2 domains identified by pfam search (Bateman, A., et al., Nucleic Acids Res. 30:276-280, 2002). Color-coded regions based on crystal structures of bovine PAP and yeast PAP (Martin, G., et al., supra, 2000; Bard, J., et al., supra, 2000). Fig. 2c: Bovine PAP 3-D structure, with key residues shown in stick form (adapted from Martin, G., et al., supra, 2000; Bard, J., et al., supra, 2000). Created by Rasmol based on pdb file 1F5A (for bovine PAP). Fig. 2d: Amino acid sequence alignment of GLD-2 and PAP core regions based on ClustalW program (Thompson, J.D., et al., Nucleic Acids Res. 22:4673-4680, 1994) and polβ superfamily analyses (Gough, J., et al., J. Mol. Biol. 313:903-919, 2001). The amino acid sequences displayed in Fig. 2d for *Hs*PAP, *Dm*PAP, *Sc*PAP, *Ce*PAP, and GLD-2 are listed in the sequence listing as SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, and SEQ ID NO:5, respectively. Mutants designated below. Red, catalytic residues; green, required for ATP binding. Fig. 2e: Unrooted tree of GLD-2 and homologs, created with PHYLIP program (Felsenstein, J., Phylogeny Interference Package, Department of Genetics, University of Washington, Seattle, WA, 1993), based on ClustalW alignment using parsimony. Species are: Ce, *C. elegans;* Dm, *Drosophila;* Hs, human; Mm, mouse; Os, rice; Sp, *S. pombe;* At, *Arabidopsis.* Only homologs with E-value less than $1e^{-10}$.in the first PSI blst were used; tree was built using the catalytic and central domain sequences as in 2d. **, Cid1 and GLD-2 both function in cell cycle control; functions of others are unknown.--

Please replace paragraph [0025] on page 11 of the application with the following amended paragraph:

--Fig. 11. Amino acid sequence alignments of putative PAPs. (A) Ribbon diagram of bovine PAP 3D structure in complex with 3'dATP (gray molecule in the center), with key residues shown in stick form. Created by Rasmol based on PDB file 1F5A (for bovine PAP, Doublie, S., EMBO J. 19:4193-4203, 2000). (B) Multiple

sequence alignment of the putative catalytic region of proteins tested in the tethered assay (the displayed sequences for Ce1 GLD-2, Mm1, Hs1, Ce2, At1, Hs2, and Bovine PAP are listed in the sequence listing as SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, and SEQ ID NO:12, respectively). Color-coding of amino acids and regions used the same scheme as in (A). D608, the 608th residue (aspartate) in *C. elegans* GLD-2 that is essential for activity (Wang, L., et al., supra, 2002).--